

sequence or multiple allele differences at two or more [nearby or] adjacent nucleotide positions, or at nucleotide positions which require overlapping oligonucleotide probe sets, in multiple target nucleotide sequences are distinguished with oligonucleotide probe groups having oligonucleotide probes with target-specific portions which overlap.

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18. (Amended) A method according to claim 1, wherein multiple allele differences consisting of insertions, deletions, microsatellite repeats, translocations, or other DNA rearrangements at one or more [nearby positions] nucleotide positions which require overlapping oligonucleotide probe sets in a single target nucleotide sequence or multiple allele differences consisting of insertions, deletions, microsatellite repeats, translocations, or other DNA rearrangements at one or more [nearby positions] nucleotide positions which require overlapping oligonucleotide probe sets in multiple target nucleotide sequences are distinguished, the oligonucleotide probe sets forming a plurality of oligonucleotide probe groups, each group comprised of one or more oligonucleotide probe sets designed for distinguishing multiple allele differences selected from the group consisting of insertions, deletions, microsatellite repeats, translocations, and other DNA rearrangements at one or more [nearby positions] nucleotide positions which require overlapping oligonucleotide probe sets, wherein, in the oligonucleotide probe sets of each group, the second oligonucleotide probes have a common target-specific portion and the first oligonucleotide probes have differing target-specific portions which hybridize to a given allele in a base-specific manner, wherein, in said detecting, the labels of ligated product sequences of each group, captured on the solid support at different sites, are detected, thereby indicating a presence, in the sample, of one or more allele differences selected from the group consisting of insertions, deletions, microsatellite repeats, translocations, and other DNA rearrangements in one or more target nucleotide sequences.

19. (Amended) A method according to claim 18, wherein the oligonucleotide probe sets are designed for distinguishing multiple allele differences selected from the group consisting of insertions, deletions, and microsatellite repeats, at one or more [nearby positions] nucleotide positions which require overlapping oligonucleotide probe sets, wherein, in the oligonucleotide probe sets of each group, the second oligonucleotide probes have a common target-specific portion, and the first oligonucleotide probes have differing target-specific portions which contain repetitive sequences of different lengths to hybridize to a given allele in a base-specific manner.

C3 20. (Amended) A method according to claim 1, wherein a low abundance of multiple allele differences at multiple [nearby or] adjacent nucleotide positions, or at nucleotide positions which require overlapping oligonucleotide probe sets, in a single target nucleotide sequence, in the presence of an excess of normal sequence, or a low abundance of multiple allele differences at multiple [nearby positions] nucleotide positions which require overlapping oligonucleotide probe sets, in multiple target nucleotide sequences, in the presence of an excess of normal sequence, are distinguished, the oligonucleotide probe sets forming a plurality of oligonucleotide probe groups, each group comprised of one or more oligonucleotide probe sets designed for distinguishing multiple allele differences at a single nucleotide position, wherein one or more sets within a group share common second oligonucleotide probes and the first oligonucleotide probes have differing target-specific portions which hybridize to a given allele excluding the normal allele in a base-specific manner, wherein, in said detecting, the labels of ligated product sequences of each group captured on the solid support at different sites, are detected, thereby indicating a presence, in the sample, of one or more low abundance alleles at one or more nucleotide positions in one or more target nucleotide sequences.

C4 22. (Amended) A method according to claim 20, wherein a low abundance of multiple allele differences at multiple [nearby or] adjacent nucleotide positions, or at nucleotide positions which require overlapping oligonucleotide probe sets, in a single target nucleotide sequence, in the presence of an excess of normal sequence, or a low abundance of multiple allele differences at multiple [nearby positions] nucleotide positions which require overlapping oligonucleotide probe sets in multiple target nucleotide sequences, in the presence of an excess of normal sequence, are quantified in a sample, said method further comprising:

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providing a known amount of one or more marker target nucleotide sequences;

providing a plurality of marker-specific oligonucleotide probe sets, each set characterized by (a) a first oligonucleotide probe having a target-specific portion complementary to the marker target nucleotide sequence and an addressable array-specific portion, and (b) a second oligonucleotide probe, having a target-specific portion complementary to the marker target nucleotide sequence and a detectable reporter label, wherein the oligonucleotide probes in a particular marker-specific oligonucleotide set are suitable for ligation together when hybridized adjacent to one another on a corresponding marker target nucleotide sequence, but, when hybridized to any other nucleotide sequence

present in the sample or added marker sequences, have a mismatch which interferes with such ligation;

providing a plurality of oligonucleotide probe groups, each group comprised of one or more oligonucleotide probe sets or marker-specific oligonucleotide probe sets designed for distinguishing multiple allele differences at a single nucleotide position, including marker nucleotide sequences, wherein one or more sets within a group share a common second oligonucleotide probe and the first oligonucleotide probes have different target-specific probe portions which hybridize to a given allele or a marker nucleotide sequence excluding the normal allele, in a base-specific manner, wherein said blending comprises blending the sample, the marker target nucleotide sequences, the plurality of oligonucleotide probe sets, the plurality of marker-specific oligonucleotide probe sets, and the ligase to form a mixture;

detecting the reporter labels of the ligated marker-specific oligonucleotide sets captured on the solid support at particular sites, thereby indicating the presence of one or more marker target nucleotide sequences in the sample; and

quantifying the amount of target nucleotide sequences in the sample by comparing the amount of captured ligated products generated from the known amount of marker target nucleotide sequences with the amount of other captured ligated product generated from the low abundance unknown sample.

26. (Amended) A method according to claim 24, wherein multiple allele differences at two or more [nearby or] adjacent nucleotide positions, or at nucleotide positions which require overlapping oligonucleotide probe sets, in a single target nucleotide sequence, or multiple allele differences at two or more [nearby or] adjacent nucleotide positions, or at nucleotide positions which require overlapping oligonucleotide probe sets, in multiple target nucleotide sequences are distinguished, the oligonucleotide probe groups containing oligonucleotide probes with target-specific portions which overlap.

30. (Amended) A method according to claim 28, wherein multiple allele differences at two or more [nearby or] adjacent nucleotide positions, or at nucleotide positions which require overlapping oligonucleotide probe sets, in a target nucleotide sequence or multiple allele differences at two or more [nearby or] adjacent nucleotide positions, or at nucleotide positions which require overlapping oligonucleotide probe sets, in multiple target nucleotide sequence are distinguished, the oligonucleotide probe groups containing probes with target-specific portions which overlap.